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UniProtKB/Swiss-Prot entry Q9U1H8

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Entry history

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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Entry information

Entry name	FACE2_DROME
Primary accession number	Q9U1H8
Secondary accession numbers	Q8SZZ3 Q9VRM4
Integrated into Swiss-Prot on	April 27, 2001
Sequence was last modified on	August 15, 2003 (Sequence version 3)
Annotations were last modified on	July 22, 2008 (Entry version 52)

Name and origin of the protein

Protein name	CAAX prenyl protease 2
Synonyms	EC 3.4.22.-
	Prenyl protein-specific endoprotease 2
	Farnesylated proteins-converting enzyme 2
	FACE-2
	Protein severas
Gene name	Name: Sras
	ORFNames: CG4852
From	Drosophila melanogaster (Fruit fly) [TaxID: 7227]
Taxonomy	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Sophophora.
Protein existence	2: Evidence at transcript level;

References

[1] NUCLEOTIDE SEQUENCE [MRNA].
Weinzierl-Hinum A., Toeroek I., Kiss I., Farkas R., Mechler B.M.;
"The severas gene of Drosophila encodes a CAAX-protease and acts as a tumour suppressor.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

[2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=Berkeley;
DOI=10.1126/science.287.5461.2185; PubMed=10731132 [NCBI, ExPASy, EBI, Israel, Japan]

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., ▩ , Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).

[3] GENOME REANNOTATION.
PubMed=12537572 [NCBI, ExPASy, EBI, Israel, Japan]
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., ▩ , Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

[4] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN=Berkeley;
TISSUE=Embryo;
PubMed=12537569 [NCBI, ExPASy, EBI, Israel, Japan]
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H., Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).

Comments

- *FUNCTION*: Proteolytically removes the C-terminal three residues of farnesylated and geranylated proteins *(By similarity)*.
- *SUBCELLULAR LOCATION*: Endoplasmic reticulum membrane; Multi-pass membrane protein *(By similarity)*.
- *SIMILARITY*: Belongs to the peptidase U48 family [view classification].

Copyright

Cross-references

Sequence databases

	AJ252068; CAB64383.1; ALT_INIT; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
EMBL	AE014296; AAF50770.3; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AY069692; AAL39837.1; -; mRNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
RefSeq	NP_524673.3; -.	
UniGene	Dm.1874	

3D structure databases

ModBase	Q9U1H8.

Protein family/group databases

MEROPS	U48.002; -.

Enzyme and pathway databases

BioCyc	DMEL-XXX-02:DMEL-XXX-02-015306-MON; -.

Organism-specific databases

FlyBase	FBgn0029121; Sras.

Gene expression databases

ArrayExpress	Q9U1H8; -.
GermOnline	CG4852; Drosophila melanogaster.

Ontologies

GO:0005789; Cellular component: endoplasmic reticulum membrane *(inferred from electron annotation from UniProtKB-SubCell)*.

GO	QuickGo view.

Family and domain databases

InterPro	IPR003675; Abi. Graphical view of domain structure.
Pfam	PF02517; Abi; 1. Pfam graphical view of domain structure.
BLOCKS	Q9U1H8.

Genome annotation databases

Ensembl	CG4852; Drosophila melanogaster. [Contig view]
GeneID	44002; -.
KEGG	dme:Dmel_CG4852; -.
NMPDR	fig|7227.3.peg.8248; -.

Phylogenomic databases

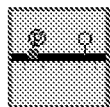| HOGENOM	Q9U1H8; -.

Other

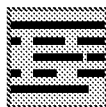| ProtoNet	Q9U1H8.
UniRef	View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Complete proteome; Endoplasmic reticulum; Hydrolase; Membrane; Transmembrane.

Features

Feature table viewer   Feature aligner

Key	From	To	Length	Description	FTId
CHAIN	1	302	302	CAAX prenyl protease 2.	PRO_0000194832
TRANSMEM	27	47	21	*Potential.*	
TRANSMEM	64	84	21	*Potential.*	
TRANSMEM	104	124	21	*Potential.*	
TRANSMEM	171	191	21	*Potential.*	
TRANSMEM	212	232	21	*Potential.*	
TRANSMEM	236	256	21	*Potential.*	
TRANSMEM	268	288	21	*Potential.*	
CONFLICT	94	95		KL -> NV (in Ref. 1; CAB64383).	
CONFLICT	122	122		I -> M (in Ref. 1; CAB64383).	
CONFLICT	138	138		D -> H (in Ref. 1; CAB64383).	

Sequence information

Length: 302 AA [This is the length of the unprocessed precursor]

Molecular weight: 34415 Da [This is the MW of the unprocessed precursor]

CRC64: 84A9EE949F1993C3 [This i: a checksum on the sequence]

```
         10         20         30         40         50         60
MKNLSETEAE VTMQENVVHE SLPQIPVATS VSCCFVLAVL YVGSLYIWST KHNRDHPTTV

         70         80         90        100        110        120
KRRFASVSMV MLAAPFFVYF FSSPELLSRV PFPKLLGLRL EGLWQAVVIP YSLTVLLFLG

        130        140        150        160        170        180
PIFVNMQNES VRSYFDLDYW RGSFGSIIWV RNHVIAPLSE EFVFRACMMP LILQSFSPLV
```

```
          190        200        210        220        230        240
     AVFITPLFFG VAHLHHIAER LSLGVELSTA LLIGLFQFIY TTLFGFYSAF LFARTGHVMA

          250        260        270        280        290        300
     PILVHAFCNH MGLPDLQDLW QQDLWRRVVA IILYLAGFVG WMFLVPLATD PSIYDNTLYW
```

NA   Q9U1H8 in
                                                                      FASTA format

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BLAST   BLAST submission on ExPASy/SIB or at NCBI (USA)

ScanProsite, MotifScan

NPSA Sequence analysis tools

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

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